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Run
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                            239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein search, using sw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     December 13, 2002, 21:07:08; Search time 26 Seconds (without alignments) 86.143 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112892 seqs, 41476328 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 ,
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293
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Match
SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HRDIKAGNILLLEKIEHDDI.....EWHRTTKMSTAGTYAWMAPE
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                                                                                                                                                                                                               M3K2_HUMAN
M3K2_HUMAN
M3KC_HUMAN
M3KC_ROUSE
M3KC_RAST
BCK1_YEAST
BCK1_YEAST
BCK1_YEAST
BCK1_YEAST
BCK1_YEAST
BCK1_GUNSE
RMIL_AVEVR
KRAB_HUMAN
RMIL_COTJA
RKAB_HUMAN
RMIL_COTJA
SK6_BRAOT
NK1_SCHPO
KI15_CAREL
CC15_YEAST
KCT1_ARATH
KCT1_ARATH
RGC1_CANAL
PGDR_MOUSE
PGDS_RAT
PGDS_HUMAN
PGDS_MOUSE
SPS1_YEAST
SPK1_YEAST
VGR1_HUMAN
PHY1_CERPU
ST24_HUMAN
MKK2_YEAST
FGR3_MOUSE
CEK2_CHICK
FGR3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112892
P80192 homo sapien Q02779 homo sapien Q12852 homo sapien Q60700 mus musculu Q63796 rattus norv Q01389 saccharomyc Q10056 schizosacch P28028 mus musculu p10533 avian rousp15056 homo sapien Q04982 gallus gallus gall P34908 coturnix co Q09092 brassica ol P38692 saccharomyc Q10407 schizosacch p34891 caenorhabdi P34891 caenorhabdi P34891 caenorhabdi P365622 mus musculu P20786 rattus norv P16234 homo sapien P36618 mus musculu P008458 saccharomyc P25848 ceratodon p Q9y6e0 homo sapien P3491 saccharomyc P15848 ceratodon p Q9y6e0 homo sapien P3491 saccharomyc P16459 gallus gall P26607 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
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45	44	43	42	41	40	39	38	37	36	35	34
93	93	94	94	94	95	95	95	95	95	95	95
31.7	31.7	32.1	32.1	32.1	32.4	32.4	32.4	32.4	32.4	32.4	32.4
426	402	1336	1333	393	1106	1087	822	822	822	819	812
Н	Н	-	Н	1	_	۳	Н	-	_	μ	1
ST25_HUMAN	KROS_AVISU	VGR1_RAT	VGR1_MOUSE	M3K7_DROME	PGDR_HUMAN	PGDS_XENLA	FGR1_RAT	FGR1_MOUSE	FGR1_HUMAN	FGR1_CHICK	FGR1_XENLA
000506 nomo sapien		P53/6/ rattus norv	P35969 mus muscuru	P83104 drosophita	PU9619 nomo sapien	P26619 xenopus tae	Q04589 FACTUS HOLV	P16092 mus muscuru	PILISO NOMO Saprem	P21804 gailus gail	P22182 xenopus lae

ALIGNMENTS

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MSKA_HUMAN
ID M3KA_H
ID M1KO9e
DE M1KO9e
DE M1KO9e
DE M1KO9
IS JO-MAY
IS JO-MAY
IS JO-MAY
IS SEQUEN
RA Suther
RA MEDLIN
RA Katch
RA GCC -!- SI
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01-FEB-1994 (Rel. 28, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Mitogen-activated protein kinase kinase kinase
(Mixed lineage kinase 2) (Protein kinase MST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96120179; PubMed=8536694;
Dorow D.S., Devereux L., Tu G.F., Price G.,
Sutherland G.R., Simpson R.J.;
"Complete nucleotide sequence, expression,
localisation of human mixed-lineage Kinase
Eur. J. Biochem. 234:492-500(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Katoh M., Hirai M., Sugimura T., Terada M.; "Cloning and characterization of MST, a novel (putative) serine/threonine kinase with SH3 domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M3KA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAP3K10 OR MLK2 OR MST.
  PRINTS; PR00452; SH3DOMAIN. PRINTS; PR00109; TYRKINASE.
                                                         Pfam; PF00069; pkinase; 1.
                                                                                 InterPro; IPR004040; STY_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                 EMBL; X90846; CAA62351.1;
EMBL; Z48615; CAA88531.1;
PIR; S32468; S32468.
                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95249256; PubMed=7731697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                               Genew;
                                                                                                                                                                                                                                                                                                          HSSP; P11362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Colon epithelium;
MEDLINE=93238756; PubMed=8477742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 244-480 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oncogene 10:1447-1451(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HRDLKSSNILILQKVENGDLSNKILKITDFGLAREWHRTTKMSAAGTYAWMAPE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HRDIKAGNILLLEKIEHDDICNKTLKITDFGLAREWHRTTKMSTAGTYAWMAPE
                                                                                                                                                                                                                                                        600137;
                                                                                                                                                                                                                                                                       HGNC:6849; MAP3K10
                                                                                                                                                                                                 IPR001452;
                                                                                                                                                                                                                         IPR000719;
                                                                                                                                                                                                                                                                                                            1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                      Euk_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicholl J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
M3KC_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
Mitogen-activated protein kinase kinase kinase (Leucine-zipper protein kinase) (ZPK).
MAPJK12 OR ZPK.
HOMO Saria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00326; SH3; 1.
SMART; SM00221; STYKC; 1.
SROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000001; Euk_pkinase;
ProDom; PD000066; SH3; 1.
 This
                                                                                                                                                                                        Reddy U.R., Pleasure D.;
"Cloning of a novel putative protein kinase having domain from human brain.";
                                                                                                                                                                                                                                                                                                                                                                                                 Q12852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; Serine/thre
ATP-binding; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50002; SH3;
                                                                                                                                                                                 Biochem.
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                MEDLINE=94311945; PubMed=8037767;
                                                                                                                                                                                                                                            ISSUE=Teratocarcinoma;
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                             NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 HRDLKSINILILEAIENHNLADTVLKITDFGLAREWHKTTKMSAAGTYAWMAPE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLAREWHRTTKMSTAGTYAWMAPE 54
                                                               similarity).
TISSUE SPECIFICITY: Highly expressed in brain and kidney
PTM: Autophosphorylated on Ser/Thr. Phosphorylated in cyl
                                                          PTM: Autophosphorylated on Ser/Thr. Phosphor under basal conditions and dephosphorylated
                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic and
                                                                                                                                  CATALYTIC ACTIVITY: ATP + a protein =
                                                                                                                                                                      Phem. Biophys. Res. Commun. 202:613-620(1994). FUNCTION: May be an activator of the JNK/SAPK
                                  associated (By similarity).
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                      COFACTOR:
                        MAP KINASE KINASE SUBFAMILY
                                                                                                                                                          Phosphorylates beta-casein, histone 1 and myelin basic
                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
 SWISS-PROT entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    954 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               818
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98
104
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384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine/threonine-protein kinase;
                                                                                                                      Magnesium
                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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81
360
112
125
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222
405
463
464
                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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72.2%;
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G -> S (IN REF. 2).

G -> R (IN REF. 2).

V -> A (IN REF. 2).
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Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
LEUCINE-ZIPPER 1 (BY SIMILARITY).
LEUCINE-ZIPPER 2 (BY SIMILARITY).
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ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                859 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
.2e-19;
 produced through a collaboration
                                                                                                            membrane-associated
                                                                                                                                  ADP + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                     12 (EC 2.7.1.37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 954;
                                                             when membrane-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQAAGRRQPHQPALWL
                                                                                                                                  phosphoprotein
                                                                                                                                                                       pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                         a leucine
                                                                        cytosol
                                                                                                                                                           protein
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Swiss Institute of Bioinformatics Bioinformatics Institute. There

There are no restrictions

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RAN HARRA RAN HA
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Best Local S
Matches 28
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U07358; HSSP; P12931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00221; STYKC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Mitogen-activated protein kinase kinase kinase 12 (EC 2.7.1.37)
(Leucine-zipper protein kinase) (ZPK) (Dual leucine zipper bear kinase) (DLK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                   STRAIN-CD-1; TISSUB-Brain; MEDLINE-95074107; PubMed=7983011; MEDLINE-95074107; PubMed=7983011; MIDLINE-95074107; Pan G.; Fan G.; "Identification, molecular cloning, and characterization of dual leucine zipper bearing kinase. A novel serine/threonine protein that defines a second subfamily of mixed lineage kinases."; J. Biol. Chem. 269:30808-30817(1994).
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAP3K12 OR ZPK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q60700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M3KC_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                Blouin R., Beaudoin J., Bergeron "Cell-specific expression of the DNA Cell Biol. 15:631-642(1996).
                                                                                                                              STRAIN-ICR X Swiss Webster; TISSUE-Brain; MEDLINE-96365388; PubMed-8769565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234
    PHOSPHORYLATION, MEDLINE=96279269;
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLAREW-HRTTKMSTAGTYAWMAPE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  600447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HRDLKSPNML----ITYDDV----VKISDFGTSKELSDKSTKMSFAGTVAWMAPE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC:6851; MAP3K12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00107; PROTEIN_KINASE_ATP; PS00108; PROTEIN_KINASE_ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P70286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR004040; STY_pkinase.
IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000719; Euk_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA67343.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366
139
152
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668
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93188
                         AND
    NND MUTAGENESIS PubMed=8663324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 124.5;
Pred. No. 1.1e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (BY SIMILAR BY SIMILARITY. POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0E5209792C5C6F05 CRC64;
                                                                                           P.,
ZPK
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                           LYS-185
                                                                                         Nadeau A
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7;
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                                AND
                                                                                         A., Grondin G.;
n adult mouse ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zipper bearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                859;
                                                                                           tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                      kinase
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Best Local
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EMBL; U23789;
HSSP; P12931;
                                                                                                                      CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>.</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mata M., Merritt S.E., Fan G., Yu G.G., Holzman L.B.; "Characterization of dual leucine zipper-bearing kinase, a mixed
                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The European Bioinformatics Institutions as long use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                      pfam; pF00069; pkinase; 1.
proDom; pD000001; Euk_pkinase; 1.
SMART; SM00221; STYKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
                                                                                      CONFLICT
                                                                                                                                                                                                                                                                    Phosphorylation;
                                                                                                                                                                  MUTAGEN
                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                           NP_BIND
                                                                                                                                                                                                                                                                                           Transferase;
                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR004040; STY_pkinase
InterPro; IPR002290; Ser_thr_pkin
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000719; Euk_p
                                                                                                            CONFLICT
                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                               MUTAGEN
267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Within the nervous system, predominantly expressed in neurons enriched in synaptic terminals.
PTM: Autophosphorylated on Ser/Thr. Phosphorylated in cytosol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: Magnesium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: ATP + a protein = ADP + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        under basal conditions and dephosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAP KINASE KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      testis, gastrointestinal tract,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylates beta-casein, histone 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                    HRDIKAGNILLLEKIEHDDICNKTLKITDFGLAREW-HRTTKMSTAGTYAWMAPE
HRDLKSPNML - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-profit institutions as long and this statement is not removed.
                                                     Similarity
                                                                                                                                                                                                                                                                                                                              PS00107; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                       PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                   PS00108; PROTEIN_KINASE_ST;
                                                                                                                                                                                                                           185
269
56
                                                                                                                                                                                                                                                            164
                                            Conservative
                                                                                                                                                                                                                                                                                           Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                      1FMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                AAA57280.1;
AAB17123.1;
                                                                                   185
69
671
701
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185
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192
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193
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96083
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                                                                                                                                                                                                                                                                                Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                               Euk_pkinase.
                                                    42.5%; 50.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressed
                                                                                                                                                                                                                                                                                                                                                                         thr_pkinase
                                                                                        MW;
                                                                                                K->A: NO CATALYTIC ACTIVITY.
E->A: NO CHANGE.
V -> A (IN REF. 2).
KL -> NV (IN REF. 2).
S -> T (IN REF. 2).
EQ -> DE (IN REF. 2).
EQ -> D (IN REF. 2).
N -> D (IN REF. 2).
                                             11;
                                                                                                                                                                                                                                                                                    Membrane
                                                                                                                                                                                                      POLY-PRO.
POLY-PRO.
 -VKISDFGTSKELSDKSTKMSFAGTVAWMAPE 313
                                             Pred. No. 1.26
l; Mismatches
                                                          Score 124.5;
Pred. No. 1.
                                                                                                                                                                                           POLY-GLU
                                                                                                                                                                                                                             POLY-GLY
                                                                                                                                                                                                                                                            ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                        PROTEIN
                                                                                        CFECF1D34F889ABB CRC64;
                                                                                                                                                                                                                                       SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in brain, kidney, lu
t, stomach, liver and
                                                                                                                                                                                                                                                                         KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and membrane-associated
                                                                                                                                                                                                                                                                                                                               FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no rest
                                                         .2e-07
                                                                    ВB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage
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                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              when
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                                                                    Length
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL outstation
                                                                     888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                              9,
                         54
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
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δÃ
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                                                                                                         Matches
                                                                 Query Match
Best Local
                                                                                                                                 Phosphorylation; J
DOMAIN 158
NP_BIND 164
BINDING 185
ACT_SITE 269
DOMAIN 56
DOMAIN 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M3KC_RAT
Q63796;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mitogen-activated protein kinase kinase kinase 12
                                                                                                         DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                      PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00108; PROTEIN_KINASE_ST; PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                          Transferase;
                                                                                                                                                                                                                                                                                              SMART; SM00221;
                                                                                                                                                                                                                                                                                                                      Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000719; InterPro; IPR004040;
                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                               entities
                                                                                                                                                                                                                                                                                                                                                                                                                                             modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEKK and MUK.";
Oncogene 12:641-650(1996).
-!- FUNCTION: May be an ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hirai S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96226099; PubMed=8637721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAP3K12 OR MUK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MAPK-upstream kinase) (MUK).
 267
                        1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLAREW-HRTTKMSTAGTYAWMAPE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: Autophosphorylated on Ser/Thr. Phosphorylated in cytosol under basal conditions and dephosphorylated when membrane-associated (By similarity).

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MAP KINASE KINASE KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \begin{array}{ll} {\tt COFACTOR: Magnesium.} \\ {\tt SUBCELLULAR\ LOCATION: Cytoplasmic\ and\ membrane-associated\ (By)} \\ \end{array} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: ATP + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylates beta-casein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: May be an
HRDLKSPNML----ITYDDV-----VKISDFGTSKELSDKSTKMSFAGTVAWMAPE 313
                                                                                                                                                                                                                                                                                                                                                                            P12931; 1FMK.
                                                                                                                                                                                                                                                                                                                                                                                       D49785; BAA08621.1;
                                                                 Similarity
                                                                                                                                                                                                                                                                                                          PD000001;
                                                                                                                                                                                                                                                                                                                                                                                                                           non-profit institutions as long
and this statement is not removed
requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                 IPR002290; Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Izawa M.,
                                                    Conservative
                                                                                                                                                                                                                                        Serine/threonine-protein kinase; ATP-binding;
                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the JNK pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                              STYKC;
                                                                                                                                                                                                                                                                                                        Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40,
                                                                                                                                              399
172
185
269
671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                 42.5%;
                                                                                                         96307
                                                                                                                                                                                                                                                                                                                                               Euk_pkinase.
STY_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Osada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activator of the JNK/SAPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S., Spyrou
thway by dis
                                                                                                         MW;
                                                                                                                                            ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
POLY-GLY.
POLY-PRO.
                                                                Score 124.5;
Pred. No. 1.2
                                                                                                                   POLY-GLU
                                                                                                                                  POLY-PRO.
                                                                                                                                                                                                               PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                         52AD964006BAE149 CRC64;
                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       histone 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rou G., Ohno S.;
distantly related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         888
                                                                                                                                                                                                                                                                               FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                 .2e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP + a phosphoprotein.
                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAPK pathway. myelin basic
                                                                           Length
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                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                              888;
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BCK1_yeast

ID BCK1_yeast

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01-CCT-1993 (Rel. 27, Created)
01-CCT-1993 (Rel. 27, Last sequence update)
01-CCT-1993 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Serine-/threonine protein kinase BCKI/SIKI/SSP31 (EC 2.7.-.-).
Serine-/threonine protein kinase BCKI/SIKI/SSP31 (EC 2.7.-.-).
BCKI OR SIKI OR SSP31 OR LAS3 OR YJL095W OR J0906.
BCKI OR SIKI OR SSP31 OR LAS3 OR YJL095W OR J0906.
BCKATYOTA; Fungi; ASCOMYCCTA; Saccharomycotina; Saccharomycetes;
Eukaryota; Fungi; ASCOMYCCTA; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-92186847; PubMed-1545797;

MEDLINE-92186847; PubMed-1545797;

Costigan C., Gehrung S., Snyder M.;

"A synthetic lethal screen identifies SLK1, a n
homolog implicated in yeast cell morphogenesis

Mol. Cell. Biol. 12:1162-1178(1992).
                                                                                                                                                                                                                                             entities re
or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BCKI) bypass the requirement for a Saccharomyces kinase C homolog.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Irie K., Araki H., Oshima Y.; "A new protein kinase, SSP31, modulating the SMP3 gene-product involved in plasmid maintenance in Saccharomyces cerevisiae."; Gene 108:139-144(1991).
                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae chromosome X including the BCK1 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miosga T., Boles E.,
Zimmermann F.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCK1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cusick M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yeast 10:1481-1488(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92107166; PubMed=1729597;
Lee K.S., Levin D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=EG123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95176706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92104496; PubMed=1840547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN A SIGNAL TRANSDUCTION PATHWAY THAT PLAY A ROLE IN YEAST CELL MORPHOGENESIS AND CELL GROWTH. THIS PATHWAY SEEMS TO STARTS BY SMP3; THEN INVOLVE THE KINASE PKC1 THAT MAY ACT ON THIS KINASE. BCK1 PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPK1 KINASE.

SUBCELLULAR LOCATION: Cytoplasmic (Potential).

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

MAP KINASE KINASE KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATES MKK1 AND MKK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INVOLVE THE KINASE PKC1
                          M84389;
D10389;
X60227;
X77923;
Z49370;
Z49369;
                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell. Biol. 12:172-182(1992)
                                                                                                                                                                                                                                          non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF 602-1104 FROM N.A.
                                                    ; -; NOT_ANNOTATED_CDS.
; BAA01226.1; -.
; CAA42788.1; -.
; CAA54896.1; -.
; CAA89389.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    function analysis of a 9.74 kb fragment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=7871887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schaaff-Gerstenschlaeger I., Schmitt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WHICH THEMSELVES PHOSPHORYLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLK1, a novel protein kinase
hogenesis and cell growth.";
                                                                                                                                                                                                                                                                                                                                                                     There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein kinase
cerevisiae pro
                                                                                                                                                                                                                                                                                                                                                                  restrictions
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Best Local
                                                                                                                                                                      SHK2_SCHPO STANDARD; PRT; 589 AA.
Q10056;
Q1-FEB-1996 (Rel. 33, Created)
G1-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase shk2 (EC 2.7.1.-).
SHK2 OR SPACIFS.09C.
                                                                                                                                                                                                                                                                                                                   1301 HRDMKADNLLL----DQDGIC----KISDEGISRKSKDIYSNSDMTMRGTVFWMAPE 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
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BINDING
                                                                                                                                                                                                                                                                  SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00107; PROTEIN_KINASE_ATP; 1
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom;
                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                 Yang P., Kansra S., Pimental R.A., Gilbreth M., Marcus S.; 
"Cloning and characterization of shk2, a gene encoding a novel p21-
activated protein kinase from fission yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                         SEQUENCE FROM N.A. MEDLINE-98325061; PubMed-9660817;
                                                                                                                            Schizosaccharomyces.
 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             Local
                        Biol. Chem. 273:18481-18489(1998).
                                                                                                                                                                                                                                                                                                                              ; S20117; S20117.
; S22285; S22285.
; JQ1118; JQ1118.
; JQ1432; JQ1432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; P24941; 1CKP.
S0003631; BCK1.
                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD000001; Euk_pkinase; 1.
                                                            Kansra S., Pimental R.A.,
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                  AA; 164194
                                                                                                                                                                                                                                                                                                                                                                             37.0%;
43.9%;
                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY T -> P (IN BCK1-19; F I -> K (IN BCK1-11; F I -> K (IN BCK1-11; F I -> K (IN BCK1-10; F I -> T (IN BCK1-20; F -> I (IN REF: 3).

E -> V (IN REF: 3).
E -> V (IN REF: 3).
N -> P (IN REF: 3).
N -> P (IN REF: 3).
N -> A (IN REF: 3).
N -> A (IN REF: 3).
N -> A (IN REF: 3).
N -> KYPQTPSYYUDR -> STPKIS -> V (IN REF: 3).
N -> G (IN REF: 3).
N -> R (IN REF: 3).
                                                                                                                                                                                                                                                                                                                                                                                                                              ADA -> RDR (IN REF. 5).

RPVPPDSSYEFIQDGLNGK -> VPIAHTSSYRMDLTVKIN
H (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                              Score 108.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  D586C3A497A5BB33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            .9e-05;
                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STPKPRVITMTE (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y PKC) (POTENTIAL).

ACTIVATION).

ACTIVATION).

ACTIVATION).

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ACTIVATION).
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                          Length 1478;
                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                   Gaps
Query Match
                                                                                                     DOMAIN
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SOUTH THE TEXT OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RA Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Bgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Miblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Janer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RT "The genome sequence of Schizosaccharomyces pombe.";
RT Nature 415:871-880 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U45981; AAA87575.1; -. EMBL; Z68136; CAA92237.1; -. HSSP; Q63450; IA06.
                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS50011; PROTEIN_KINASE_DOM; PROSITE; PS00108; PROTEIN_KINASE_ST; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21848401; PubMed=11859360;
                                                                  SEQUENCE
                                                                                                                                     BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: FORMS AN ACTIVATED COMPLEX WITH GTP-BOUND RAS-LIKE CDC42. PARTICIPATES IN RAS-DEPENDENT MORPHOLOGICAL CONTROL AN MATING RESPONSE PATHWAYS.
MATING RESPONSE PATHWAYS.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 CRIB DOMAIN. SIMILARITY: CONTAINS 1 PH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STE20 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00285; PBD; 1.
SM00233; PH; 1.
SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;100000dd
                                                                                                                                                                                                                                                                                                                                                                                                                                   PS50108; CRIB; 1.
PS50003; PH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000719; Euk_pkinase
                                                                                                                                                                                                                                                                                                     0108; PROTEIN_KINASE_ST; 1.
Serine/threonine-protein kinase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PBD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euk_pkinase;
                                                                  66765 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ser_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAKbox/Rhobndng.
34.5%; Score 101; DB 1; Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thr_pkinase.
                                                                                                    BY SIMILARITY
                                                                                                                          PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                         CRIB.
                                                                                                                                                                                                                                                                           PН
                                                                  CA8E2190925EC231 CRC64;
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             Query Match
Best Local
 Matches
                                                           BINDING
ACT_SITE
SEQUENCE
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01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; Proto-oncogene;
ATP-binding; Chromosomal translocation.
                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miki T., Fleming T.P., Crescenzi M., Molloy C.J., Blam S.B.,
Reynolds S.H., Aaronson S.A.;
"Development of a highly efficient expression cDNA cloning system:
application to oncogene isolation.";
proc. Natl. Acad. Sci. U.S.A. 88:5167-5171(1991).
-1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS
FROM THE CELL MEMBRANE TO THE NUCLEUS.
-1- FUNCTION: MAY PLAY A ROLE IN THE POSTSYNAPTIC RESPONSES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B-RAF proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-)
                                                                                                                         DOMAIN
                                                                                                                                                                                                                                 SMART; SM00221; STYKC;
                                                                                                                                                                                                                                                                            Interpro; IPR000719;
Interpro; IPR004040;
Interpro; IPR002290;
                                                                                                                                                                                                                                                                                                                                                         PIR; A40951; TVMSBF.
                                                                                                                                                                                                                                                                                                                                                                       EMBL; M64429; AAA37320.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Fragment).
BRAF OR B-RAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRAB_MOUSE
                                                                                                                                                                                                                                                                                                                            MGD; MGI:88190; Braf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGL-AREWHRTTKMST-AGTYAWMAPE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: PARTICIPATES IN A CHROMOSOMAL TRANSLOCATION THAT PRODUCES A TIFIA-BRAF (T18) ONCOGENE ORIGINALLY ISOLATED FROM A FURFURAL-INDUCED HEPATOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIL/RAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIPPOCAMPAL NEURON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HRDIKSDNVLL-----DNSGN--IKITDFGFCARLSNRTNKRVTMVGTPYWMAPE 479
 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
             Similarity
                                                                                                                                                                                                                                               PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .271351;
                                                           328 AA;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                               pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=2052597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Rodentia;
             34.1%;
                                                           36986 MW;
                                                                                                                                                                                                                                                                           Euk_pkinase.
STY_pkinase.
Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.8%;
 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 5; Mismato
             Score 100; DB 1; Length 328; Pred. No. 4.3e-05;
                                                                         PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                           67A2EBFB78A78E3D CRC64;
 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328
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12;
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 9;
 Indels
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 16;
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Gaps
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RMIL_AVIII

RMIL_A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RMIL_AVII1 STANDARD; P10533; Q85612; Q85613; Q85614; Q1-JUL-1989 (Rel. 11, Created)
                                                                                                                                                        NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00221; STYKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S01645; TVFVMI. HSSP; P08631; 1AD5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X13744; CAA32008.1; ALT_SEQ. EMBL; X13438; CAA31790.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A novel oncogene related to c-mil is transduced in chicken neuroretina cells induced to proliferate by infection with an avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marx M., Eychene A., Laugier D., Bechade C., Crisanti P., Dezelee P., Pessac B., Calothy G.;
"A novel oncogene related to c-mil is transduced in chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89160254; PubMed=2537952;
Eychene A., Marx M., Dezelee P., Calothy G.;
"Complete nucleotide sequence of IC10, a retrovirus containing the
Rmil oncogene transduced in chicken neuroretina cells infected with
avian retrovirus RAV-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Avian retrovirus IC10.
Viruses; Retroid viruses; Retroviridae; Avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine/threonine-protein kinase transforming protein Rmil (EC 2.7.1.37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1989 (Rel. 11, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                 Polyprotein; Serine/threonine-protein kinase; Transferase; Oncogene;
                                                                                                                                                                                                                                                                                                                    PROSITE; PS00107; PROTEIN_KINASE_ATP; 1
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P08631, 1AD5.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR004040; STY_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89091077; PubMed=2850163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 17:1250-1250(1989).
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                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lymphomatosis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLA---REW---HRTTKMSTAGTYAWWAPE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONG MIL/RAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) J. 7:3369-3373(1988).
CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein
MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-R-MIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLYPROTEIN.
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                                                                                                                                                                  67
93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                   186
                                                                                                 41023 MW;
      34.1%;
Score 100; DB 1;
Pred. No. 4.8e-05;
                                                                                                                            PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                 E137AFCDECB9398A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
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                                  Length 367;
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RESULT 10

RASIL_A

RMIL_A

AC P27966

DT 01-AUG

DT 01-AUG

DT 01-BUG

DT 01-AUG

DT 01-AUG

DT 01-AUG

CC 2.

RN [1]

RP SEQUEN

RA FEIGUEN

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CC -!- CI

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                                                                                                           Query Match
Best Local :
                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P27966;
01-AUG-1992 (Rel. 23, C
01-AUG-1992 (Rel. 23, I
15-JUN-2002 (Rel. 41, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-91251215; PubMed-1645786;
MEDLINE-91251215; PubMed-1645786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Avian rous-associated virus Viruses; Retroid viruses; ReROB_TaxID=11950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine/threonine-protein (EC 2.7.1.37).
                                                                                                                                                                                                 NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMIL_AVEVR
                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A40341; TVFVMR.
HSSP; P08631; 1AD5.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR004040; STY_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and c-Rmil in chicken virus type 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Virol. 65:3633-3640(1991).
-!- CATALYTIC ACTIVITY: ATP + a
-!- MISCELLAREOUS: THIS PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00221; STYKC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M62407; AAA42549.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Common mechanism of retrovirus activation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marx M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184
                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                       Polyprotein; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom;
                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                    DOMAIN
200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIL/RAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HRDIKAGNILLLEKIEHDDICNKTLKITDFGLA---REW---HRTTKMSTAGTYAWMAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HRDLKSNNIFL----HEDL---TVKIGDFGLATVKSRWSGSHQFEQLS--GSILWMAPE 233
                                       HRDIKAGNILLLEKIEHDDICNKTLKITDFGLA---REW---HRTTKMSTAGTYAWMAPE 54
HRDLKSNNIFL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                                                                                                                                                                                                                                                                                                                                                                                                       PD000001; Euk_pkinase; 1.
                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                 PS00107: PROTEIN_KINASE_ATP;
PS00108: PROTEIN_KINASE_ST; 1
PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                         83
89
109
202
450 AA;
                                                                                                                                                                                                                                                                                                  01107; PROTEIN_KINASE_ATP; 1.
01108; PROTEIN_KINASE_ST; 1.
0011; PROTEIN_KINASE_DOM; 1.
Serine/threonine-protein kinase;
                                                                                        Conser
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97
109
202
50313 .
                                                                                        vative
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Last annotation update)
ein kinase transforming
                                                                                                             34.18;
43.38;
    HEDL - - - TVKIGDFGLATVKSRWSGSHQFEQLS - - GSILWMAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroretina cells
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Retroviridae;
                                                                                                                                                                              MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9;
                                                                                                                                                                                                 PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                        9;
                                                                                                             Score 100;
Pred. No.
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                                                                                                                                                                              6581AAF2253CB622 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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IS SYNTHESIZED
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                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ion and transduction of c-mil infected with Rous-associated
                                                                                                               6e-05;
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                                                                                                                                    DB
                                                                                                                                  μ.
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                                                                                                                                                                                                                                                                                                                   Transferase;
                                                                                        9;
                                                                                                                                    Length 450;
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A R-MIL-ENV
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                                                                                                                                                                                                                                                                                                                Oncogene;
                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G.,
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                                                                                          Gaps
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RESULT

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KRAB_HUMAN

ID KRAB_HUMAN

AC PISSOS;

DT 01-NOV-1990

DT 01-NOV-1995

DT 01-N
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B-Raf proto-oncogene serine/threonine-protein kina:
(p94) (v-Raf murine sarcoma viral oncogene homolog
BRAF OR BRAFI OR RAFBI.
Homo sapiens (Human).
Eukaryota: Metarro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIJINE-9113728; PubMed=2284096; Sithanandam G., Kolch W., Duh F.-M., Rapp U.R.; Complete coding sequence of a human B-raf cDNA and detement of the sequence of a human B-raf contains with isozyme specific antibodies."; Oncogene 5:1775-1780(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 438-765 FROM N.A.
MEDLINE-88302178; PubMed-3043188;
Ikawa S., Fukui M., Ueyama Y., Tamaoki N.,
"B-raf, a new member of the raf family, is
rearrangement.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stephens R.M.,
Morrison D.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOI. Cell. Biol. 8:2651-2654(1988).
-I- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS FROM THE CELL MEMBRANE TO THE NUCLEUS.
-I- FUNCTION: MAY PLAY A ROLE IN THE POSTSYNAPTIC RESPONSES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein and
                                                                                                                                                                                                                                                                                                PIR; A31850; TVHUBF.
PIR; S13798; S13798.
HSSP; P04049; 1FAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92375040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                 Pfam; PF00069; pkinase; 1.
Pfam; PF00130; DAG_PE-bind; 1.
Pfam; PF02196; RBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95-kilodalton B-Raf serine/threonine kinase: identification of the
                                                                                                                       InterPro; IPR003116;
InterPro; IPR004040;
InterPro; IPR002290;
                                                                                                                                                                                                                                                    MIM; 164757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: CEREBROW AND TESTES.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASE:
MIL/RAF SUBFAMILY.
SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIPPOCAMPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pin and its major autophosphorylation site."; Cell. Biol. 12:3733-3742(1992).
                                                                                                                                                                                                                                                                                                                                                                         M95712; AAA35609.1; M21001; AAA96495.1;
                                                                                                                                                                                                                                                                         HGNC:1097; BRAF
PD000001; Euk_pkinase;
                               PR00008;
                                                                                                                                                                         IPR002219;
IPR000719;
IPR003116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sithanandam G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEURON
                               DAGPEDOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=1508179;
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                                                                                                                                                                                             DAG_PE-bind.
Euk_pkinase.
                                                                                                                            Ser_thr_pkinase
                                                                                                                                                                              RBD.
                                                                                                                                               STY_pkinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kinase (EC
molog B1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restrictions
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DNA
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Best Local
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01-FEB-1994
01-FEB-1994
16-OCT-2001
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NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE: PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                TISSUE=Lymphocytes, and Fibroblast;
MEDLINE=93312327; PubMed=8323553;
Calogeraki I., Barnier J.V., Eychene A., Felder M.~P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHICK
                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                             -
                                                                                                                                                                                                                       +
                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 193:1324-1331(1993).
                                                                                                                                                                                                                                                            "Genomic organization and nucleotide sequence of the coding region the chicken c-Rmil(B-raf-1) proto-oncogene."; Biochem. Biophys. Res. Commun. 193:1324-1331(1993).
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                             Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RMIL_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLA---REW---HRTTKMSTAGTYAWMAPE
                                                                                                                                                                          CATALTRIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                       PTM: PHOSPHORYLATED. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                 BINDING DOMAIN.
                                                                                                             SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
                                                                                                                                                                   TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEURAL TISSUE
                                                                                                                          MIL/RAF SUBFAMILY
                                                                                                                                                                                                                                   NEURAL CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HRDLKSNNIFL----HEDL---TVKIGDFGLATVKSRWSGSHQFEQLS--GSILWMAPE 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                               JF-2001 (Rel. 40, Last annotation update)
serine/threonine-protein kinase (EC 2.7.1.37).
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SM00455;
SM00221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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4 (Rel. 28,
1 (Rel. 40,
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234
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575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; C1; 1.
; RBD; 1.
; STYKC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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279
431
716
470
482
575
575
372
                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84490 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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Pred. No. 0.0001;
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PHOSPHORYLATION (AUTO-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP
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ATP (BY SIMILAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHORBOL-ESTER AND DAG BINDING POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
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Best Local S
Matches 26
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BINDING
ACT_SITE
VARSPLIC
                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
RMIL serine/threonine-protein kinase (
                                                                           "Quail neuroretina c-Rmil(B-raf) proto-oncogene cDNAs encode two proteins of 93.5 and 95 kDa resulting from alternative splicing. Oncogene 7:1315-1323(1992).
                                                                                                            MEDLINE-92319540; PubMed-1620546; Eychene A., Barnier J.V., Dezelee Calogeraki I., Calothy G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00109; C1; 1.
SMART; SM00455; RBD; 1.
SMART; SM00221; STYKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                          Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                  C-RMIL
                                                                                                                                                                                                                                                                                                                  COTJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X67052; CAA47436.1; ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
-!- CATALITIC POLICIES. Nuclear.
-!- SUBSCELULAR COCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND
-!- ALTERNATIVE PRODUCED BY ALTERNATIVE SPLICING.
                                                               -!- FUNCTION: MAY PLAY A ROLE IN TRANSDUCING
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                      NCBI_TaxID=93934;
                                                                                                                                                                                                Archosauria; Aves;
                                                                                                                                                                                                                                                                                                     RMIL_COTJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proto-oncogene; Transferase; Serine/threonine-protein kinase; Proto-oncogene; Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc; Alternative splicing; Zinc;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pram;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002219; DAG_PE-bind
InterPro; IPR000719; Euk_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; JN0612; JN0612.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                             1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLA---REW---HRTIKMSTAGTYAWMAPE 54
                                       NEURAL CELLS.
CATALYTIC ACTIVITY: ATP + a protein =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00069; pkinase; 1.
PF00130; DAG_PE-bind; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           806
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                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           89365
                                                                                                                                                                                                                                                                                                                                                                                                                        34.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
MISSING (IN SHORT ISOFORM)
, 8F3FA4D5274FB75C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 100; DB 1;
Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHORBOL-ESTER AND DAG BINDING CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-SER
                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                          P., Marx M., Laugier
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                                                                                                                                                                                                                                                                                                       807
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                                         ADP + a phosphoprotein.
                                                                SPECIFIC SIGNALS
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 806;
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                                                                                      splicing.";
                                                                                                                                                                                                Phasianinae;
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SOFTER TRANSPORTER TO DESCRIPTION OF THE PROPERTY OF THE PROPE
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SRK_BERK6_B
ID SRK6_B
AC Q09092
DT 01-FEB
DT 01-FEB
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DE PUTATI
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OS Brassi
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Best Local
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SMART; SM00109; C1; 1.

SMART; SM00455; RBD; 1.

SMART; SM00455; RBD; 1.

PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.

PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots. Peurosids II; Brassicales; Brassicaceae; Rrachiones (NCBI_TaxID=3712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M80846; AAA49493.1; -. EMBL; M80845; AAA49492.1; -. HSSP; P04049; 1FAR.
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                                                                                                                                                ORK6_BRAOL STANDARD; PRT; 8
Q09092;
Q1-FEB-1995 (Rel. 31, Created)
Q1-FEB-1995 (Rel. 32, Last sequence up
Q1-NOV-1995 (Rel. 32, Last annotation
putative serine/theonine kinase recep
(S-receptor kinase) (SRK).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                            614
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLA---REW---HRTTKMSTAGTYAWMAPE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIL/RAF SUBFAMILY
SIMILARITY: CONTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: PHOSPHORYLATED.
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLE...

12 binding:
122 129
122 235 280
248 28
2497 7
503
518 523
17E 513
513
513
616
5110
807 1
                                                                                                                                                                                                                                                                                                                                                                                        HRDLKSNNIFL----HEDL---TVKIGDFGLATVKSRWSGSHQFEQLS--GSILWMAPE 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF02196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR002219; DAG_PE-bind.
IPR000719; Euk_pkinase.
IPR003116; RBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR004040; STY_pkinase.
IPR002290; Ser_thr_pkir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEURAL TISSUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pkinase;
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ATP (BY SIMILAF
BY SIMILARITY:
MISSING (IN SHO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 no restrictions
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                                                                     Rosidae;
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Query Match
Best Local S
Matches 25
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SEQUENCE FROM N.A.
STRAIN=CV. S6S6; TISSUE=Stigma;
                                                                                                                                                                                                               DOMAIN
NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CV. S6S6; TISSUE=Stigma; MEDLINE=92020942; PubMed=1681543;
                                                                                                                                             CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000001; Euk_pki; SMART; SM00108; B_lectin; SMART; SM00473; PAN_AP; 1 SMART; SM00221; STYKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00069; pkinase; 1.
Pfam; PF00954; S_locus_glycop; 1.
Pfam; PF01453; Agglutinin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004040; STY_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR000858; Slocus_glycop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001480;
InterPro; IPR000719;
InterPro; IPR003609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M76647; AAA33000.1; ALT_TERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
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SIGNAL
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                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                       SEQUENCE
                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                           CARBOHYD
                                                                                                                            CARBOHYD
                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotei SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREDOMINANTLY IN THE PISTIL AND ANTHER. POLYMORPHISM: THERE ARE A NUMBER OF DIFFERENT S ALLELES IN POLYMORPHISM: THE RECOGNITION SPECIFICITY.

B. OLERACEA, POSSIBLY PROVIDING THE RECOGNITION SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restricted to the control of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B.OLERACEA, POSSIBLY PROVIDING THE RECOGNITION SPECIFICITY SIMILARITY: THE EXTRACELLULAR DOMAIN IS SIMILAR TO S-LOCUS GLYCOPROTEINS OF BRASSICA, WHILE THE INTRACELLULAR DOMAIN A SER/THR-PROTEIN KINASE RELATED TO RAF KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00107;
PS00108;
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447
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556
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Serine/threonine-protein kinase; Signal; ATP-b
e; Receptor; Glycoprotein; Self-incompatibility
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euk_pkinase;
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466
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                    34.1%;
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                  Score 100; DB 1;
Pred. No. 0.00012;
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ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
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D (GLCNAC...
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                                                                                          GLCNAC . .
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                                                                                                                                                                                                                                                                                                                                                                 SERINE/THREONINE KINASE
                                                                                                                                                                                                                                                                                             (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; ATP-binding;
                                     Length 849;
                                                                           CRC64;
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MBL outstation -
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Similarity

Conservative

Mismatches

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                                                                                                                       R Pfam; PF0066; pkinase; 1.

R PTODOM; PD00001; Euk_pkinase; 1.

R PTODOM; PD000001; Euk_pkinase; 1.

R PROSITE; SM00220; S_TKC; 1.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS001108; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00118; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00110; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS0011; PROTEIN_KINASE_ST; 1.

R PROSITE; PS0011; PROTEIN_KINASE_ST; 1.

R PROSITE; PS0011; PROTEIN_KINASE_ST; 1.

R PROSITE; PS0011; PROTEIN_KINASE, ATP-binding.

T TAINSIER 23 276 PROTEIN KINASE.

T NP_BIND 29 37 ATP (BY SIMILARITY).

T BINDING 52 52 ATP (BY SIMILARITY).

T ACT_SITE 144 144 BY SIMILARITY.

SEQUENCE 1080 AA; 117061 MW; 9989EAF315EE0B94 CRC64;
                                                                            Query Match
Best Local
                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 265:2077-2082(1994).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam: PF00069; pkinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRK1_YEAST STANDARD; PRT; 1080 AA.
p38692;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine-protein kinase NRK1 (EC 2.7.1.37) (N-rich kinase 1).
NRK1 OR KIC1 OR YHR102W.
                                                                                                                                                                                                                                                                                                                                                                                              PIR; S48944; S48944.
SGD; S0001144; KIC1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vignati D., Wilcox L., Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-DC-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94378003; PubMed=8091229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
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HRDIKAGNILLLEKIEHDDICNKTLKITDFGLAREWHRTT--KMSTAGTYAWMAPE
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                                                                            Similarity
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / AB972;
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                                                                         34.1%;
                                                           12;
                                                     Score 100; DB 1;
Pred. No. 0.00015;
2; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces.
                                                       12;
                                                                                          Length 1080;
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for
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Db 142 HRDIKAANVLITNE------GNVKLCDFGVAAQVNQTSLRRQTMAGTPYWMAPE 189

Search completed: December 13, 2002, 23:29:18 Job time: 32 secs